1638

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TRANSMITTAL FORM

(to be used for all correspondence after initial filing)

Application Number	09/529,239
Filing Date	October 27, 2000
First Named Inventor	Doutriaux
Group Art Unit	1638
Examiner Name	D. Kruse

Total Number of Pages in This Submission		**Attorney Docket Number**	A33153PCTUSA;072667.0128

ENCLOSURES *(check all that apply)*

- [ ] Fee Transmittal Form
  - [ ] Fee Attached
- [✔] Amendment / Reply
  - [ ] After Final
  - [ ] Affidavits/declaration(s)
- [ ] Extension of Time Request
- [ ] Express Abandonment Request
- [ ] Information Disclosure Statement
- [ ] Certified Copy of Priority Document(s)
- [ ] Response to Missing Parts/ Incomplete Application
  - [ ] Response to Missing Parts under 37 CFR 1.52 or 1.53

- [ ] Assignment Papers *(for an Application)*
- [ ] Drawing(s)
- [ ] Licensing-related Papers
- [ ] Petition
- [ ] Petition to Convert to a Provisional Application
- [ ] Power of Attorney, Revocation Change of Correspondence Address
- [ ] Terminal Disclaimer
- [ ] Request for Refund
- [ ] CD, Number of CD(s) _____

- [ ] After Allowance Communication to Group
- [ ] Appeal Communication to Board of Appeals and Interferences
- [ ] Appeal Communication to Group *(Appeal Notice, Brief, Reply Brief)*
- [ ] Proprietary Information
- [ ] Status Letter
- [ ] Other Enclosure(s) *(please identify below)*:

Remarks	[✔]

RESPONSE TO NOTICE TO COMPLY AND SUBMISSION OF SUBSTITUTE SEQUENCE LISTING

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm or Individual name	BakerBotts LLP 30 Rockefeller Plaza New York, NY 10112		
Signature	*[signature]*	Att Name:	Rochelle K. Seide, Ph.D.
		PTO Reg:	32,300
Date	August 10, 2001		

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, Washington, DC 20231 on this date: | August 10, 2001

Typed or printed name	Rochelle K. Seide, Ph.D.		
Signature	*[signature]*	Date	August 10, 2001
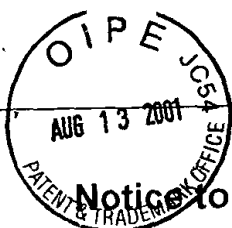
	Application No.	Applicant(s)
Notice to Comply	09/529,239	DOUTRIAUX ET AL.
	Examiner	Art Unit
	David H Kruse	1638

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
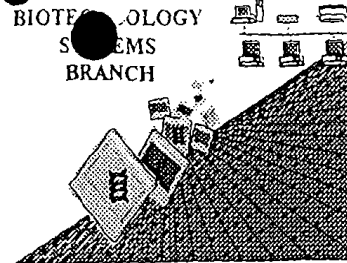PatentIn Software Program Support
    Technical Assistance...703-287-0200
    To Purchase PatentIn Software........................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/529,239_

Source: _1638_

Date Processed by STIC: _6-12-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/529,239

DATE: 06/12/2001
TIME: 13:19:50

Input Set : A:\09529239SeqList.txt
Output Set: N:\CRF3\06122001\I529239.raw

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    2 <110> APPLICANT: Doutriaux, Marie-Pascale
    3        Betzner, Andreas
    4        Freyssinet, Georges
    5        Perez, Pascal
    7 <120> TITLE OF INVENTION: METHOD FOR OBTAINING PLANT VARIETIES
   10 <130> FILE REFERENCE: A33153-PCT-USA 072667.0128
   12 <140> CURRENT APPLICATION NUMBER: US 09/529,239
C--> 13 <141> CURRENT FILING DATE: 2000-01-27
   15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06977
   16 <151> PRIOR FILING DATE: 1998-10-09
   18 <160> NUMBER OF SEQ ID NOS: 98
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ERRORED SEQUENCES

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  932 <210> SEQ ID NO: 26        Number of sequences differ:
  933 <211> LENGTH: (1385)         -1385 listed
  934 <212> TYPE: DNA              -2188 shown (see next page)
  935 <213> ORGANISM: Arabidopsis thaliana ecotype Columbia
  936 <223> OTHER INFORMATION: Clone 43
  938 <400> SEQUENCE: 26
  940 cccgggatgc agcgccagag atcgattttg tctttcttcc aaaaacccac ggcggcgact    60
  941 acgaagggtt tggtttccgg cgatgctgct agcggcgggg gcggcagcgg aggaccacga   120
  942 tttaatgtga aggaaggggga tgctaaaggc gacgcttctg tacgttttgc tgtttcgaaa   180
  943 tctgtcgatg aggttagagg aacggatact ccaccggaga aggttccgcg tcgtgtcctg   240
  944 ccgtctggat ttaagccggc tgaatccgcc ggtgatgctt cgtccctgtt ctccaatatt   300
  945 atgcataagt ttgtaaaagt cgatgatcga gattgttctg gagagaggag ccgagaagat   360
  946 gttgttccgc tgaatgattc atctctatgt atgaaggcta atgatgttat tcctcaattt   420
  947 cgttccaata atggtaaaac tcaagaaaga aaccatgctt ttagtttcag tgggagagct   480
  948 gaacttagat cagtagaaga tataggagta gatggcgatg ttcctggtcc agaaacacca   540
  949 gggatgcgtc cacgtgcttc tcgcttgaag cgagttctgg aggatgaaat gacttttaag   600
  950 gaggataagg ttcctgtatt ggactctaac aaaaggctga aaatgctcca ggatccggtt   660
  951 tgtggagaga agaaagaagt aaacgaagga accaaatttg aatggcttga gtcttctcga   720
  952 atcagggatg ccaatagaag acgtcctgat gatccccttt acgatagaaa gaccttacac   780
  953 ataccacctg atgttttcaa gaaaatgtct gcatcacaaa agcaatattg gagtgttaag   840
  954 agtgaatata tggacattgt gcttttcttt aaagtgggga aatttttatga gctgtatgag   900
  955 ctagatgcgg aattaggtca caaggagctt gactggaaga tgaccatgag tggtgtggga   960
  956 aaatgcagac aggttggtat ctctgaaagt gggatagatg aggcagtgca aaagctatta  1020
  957 gctcgtggat ataaagttgg acgaatcgag cagctagaaa catctgacca agcaaaagcc  1080
  958 agaggtgcta atactataat tccaaggaag ctagttcagg tattaactcc atcaacagca  1140
  959 agcgagggaa acatcgggcc tgatgccgtc catcttcttg ctataaaaga gatcaaaatg  1200
  960 gagctacaaa agtgttcaac tgtgtatgga tttgcttttg ttgactgtgc tgccttgagg  1260
  961 ttttgggttg ggtccatcag cgatgatgca tcatgtgctg ctcttggagc gttattgatg  1320
  962 caggtttctc caaaggaagt gttatatgac agtaaagggc tatcaagaga agcacaaaag  1380
  963 gctctaagga aatatacgtt gacagggtct acggcggtac agttggctcc agtaccacaa  1440
  964 gtaatggggg atacagatgc tgctggagtt agaaatataa tagaatctaa cggatacttt  1500
  965 aaaggttctt ctgaatcatg gaactgtgct gttgatggtc taaatgaatg tgatgttgcc  1560
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RAW SEQUENCE LISTING   DATE: 06/12/2001
PATENT APPLICATION: US/09/529,239   TIME: 13:19:50

        Input Set : A:\09529239SeqList.txt
        Output Set: N:\CRF3\06122001\I529239.raw

     966 cttagtgctc ttggagagct aattaatcat ctgtctaggc taaagctaga agatgtactt   1620
     967 aagcatgggg atatttttcc ataccaagtt tacaggggtt gtctcagaat tgatggccag   1680
     968 acgatggtaa atcttgagat atttaacaat agctgtgatg gtggtccttc agggaccttg   1740
     969 tacaaatatc ttgataactg tgttagtcca actggtaagc gactcttaag gaattggatc   1800
     970 tgccatccac tcaaagatgt agaaagcatc aataaacggc ttgatgtagt tgaagaattc   1860
     971 acggcaaact cagaaagtat gcaaatcact ggccagtatc tccacaaact tccagactta   1920
     972 gaaagactgc tcggacgcat caagtctagc gttcgatcat cagcctctgt gttgcctgct   1980
     973 cttctgggga aaaaagtgct gaaacaacga gttaaagcat ttgggcaaat tgtgaaaggg   2040
     974 ttcagaagtg gaattgatct gttgttggct ctacagaagg aatcaaatat gatgagtttg   2100
     975 ctttataaac tctgtaaact tcctatatta gtaggaaaaa gcgggctaga gttattttctt   2160
E--> 976 tctcaattcg aagcagccat agatagcg   ⟨2188⟩

                                                                     ⟶ 1385 listed.
    1013 <210> SEQ ID NO⟨ 28 ⟩
    1014 <211> LENGTH: 34
    1015 <212> TYPE: DNA
    1016 <213> ORGANISM: Artificial sequence
    1018 <220> FEATURE:
    1019 <223> OTHER INFORMATION: MSH6 specific primer 2S8 for PCR using cDNA of Arabidopsis
thaliana
    1020   ecotype Columbia   ⟶ Incorrect sequence i.d. number.
E--> 1022 <400> SEQUENCE ⟨ 26 ⟩
    1024 atcccgggtt atttgggaac acagtaagag gatt   34
    1341 <210> SEQ ID NO: 31
    1342 <211> LENGTH: 1109
    1343 <212> TYPE: PRT
    1344 <213> ORGANISM: Arabidopsis thaliana ecotype Columbia
    1345 <223> OTHER INFORMATION: Polypeptide MSH6
    1347 <400> SEQUENCE: 31
    1349 Met Gln Arg Gln Arg Ser Ile Leu Ser Phe Phe Gln Lys Pro Thr Ala
    1350 1   5   10   15
    1352 Ala Thr Thr Lys Gly Leu Val Ser Gly Asp Ala Ala Ser Gly Gly Gly
    1353   20   25   30
    1355 Gly Ser Gly Gly Pro Arg Phe Asn Val Arg Glu Gly Asp Ala Lys Gly
    1356   35   40   45
    1358 Asp Ala Ser Val Arg Phe Ala Val Ser Lys Ser Val Asp Glu Val Arg
    1359   50   55   60
    1361 Gly Thr Asp Thr Pro Pro Glu Lys Val Pro Arg Arg Val Leu Pro Ser
    1362 65   70   75   80
    1364 Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp Ala Ser Ser Leu Phe Ser
    1365   85   90   95
    1367 Asn Ile Met His Lys Phe Val Lys Val Asp Asp Arg Asp Cys Ser Gly
    1368   100   105   110
    1370 Glu Arg Ser Arg Glu Asp Val Val Pro Leu Asn Asp Ser Ser Leu Cys
    1371   115   120   125
    1373 Met Lys Ala Asn Asp Val Ile Pro Gln Phe Arg Ser Asn Asn Gly Lys
    1374   130   135   140
    1376 Thr Gln Glu Arg Asn His Ala Phe Ser Phe Ser Gly Arg Ala Glu Leu
    1377 145   150   155   160
    1379 Arg Ser Val Glu Asp Ile Gly Val Asp Gly Asp Val Pro Gly Pro Glu
    1380   165   170   175
    1382 Thr Pro Gly Met Arg Pro Arg Ala Ser Arg Leu Lys Arg Val Leu Glu

RAW SEQUENCE LISTING   DATE: 06/12/2001
PATENT APPLICATION: US/09/529,239   TIME: 13:19:50

Input Set : A:\09529239SeqList.txt
Output Set: N:\CRF3\06122001\I529239.raw

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1383              180             185             190
1385 Asp Glu Met Thr Phe Lys Glu Asp Lys Val Pro Val Leu Asp Ser Asn
1386         195             200             205
1388 Lys Arg Leu Lys Met Leu Gln Asp Pro Val Cys Gly Glu Lys Lys Glu
1389     210             215             220
1391 Val Asn Glu Gly Thr Lys Phe Glu Trp Leu Glu Ser Ser Arg Ile Arg
1392 225             230             235             240
1394 Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro Leu Tyr Asp Arg Lys Thr
1395         245             250             255
1397 Leu His Ile Pro Pro Asp Val Phe Lys Lys Met Ser Ala Ser Gln Lys
1398         260             265             270
1400 Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met Asp Ile Val Leu Phe Phe
1401     275             280             285
1403 Lys Val Gly Lys Phe Tyr Glu Leu Tyr Glu Leu Asp Ala Glu Leu Gly
1404     290             295             300
1406 His Lys Glu Leu Asp Trp Lys Met Thr Met Ser Gly Val Gly Lys Cys
1407 305             310             315             320
1409 Arg Gln Val Gly Ile Ser Glu Ser Gly Ile Asp Glu Ala Val Gln Lys
1410             325             330             335
1412 Leu Leu Ala Arg Gly Tyr Lys Val Gly Arg Ile Glu Gln Leu Glu Thr
1413         340             345             350
1415 Ser Asp Gln Ala Lys Ala Arg Gly Ala Asn Thr Ile Ile Pro Arg Lys
1416         355             360             365
1418 Leu Val Gln Val Leu Thr Pro Ser Thr Ala Ser Glu Gly Asn Ile Gly
1419     370             375             380
1421 Pro Asp Ala Val His Leu Leu Ala Ile Lys Glu Ile Lys Met Glu Leu
1422 385             390             395             400
1424 Gln Lys Cys Ser Thr Val Tyr Gly Phe Ala Phe Val Asp Cys Ala Ala
1425         405             410             415
1427 Leu Arg Phe Trp Val Gly Ser Ile Ser Asp Asp Ala Ser Cys Ala Ala
1428         420             425             430
1430 Leu Gly Ala Leu Leu Met Gln Val Ser Pro Lys Glu Val Leu Tyr Asp
1431     435             440             445
1433 Ser Lys Gly Leu Ser Arg Glu Ala Gln Lys Ala Leu Arg Lys Tyr Thr
1434     450             455             460
1436 Leu Thr Gly Ser Thr Ala Val Gln Leu Ala Pro Val Pro Gln Val Met
1437 465             470             475             480
1439 Gly Asp Thr Asp Ala Ala Gly Val Arg Asn Ile Ile Glu Ser Asn Gly
1440             485             490             495
1442 Tyr Phe Lys Gly Ser Ser Glu Ser Trp Asn Cys Ala Val Asp Gly Leu
1443         500             505             510
1445 Asn Glu Cys Asp Val Ala Leu Ser Ala Leu Gly Glu Leu Ile Asn His
1446         515             520             525
1448 Leu Ser Arg Leu Lys Leu Glu Asp Val Leu Lys His Gly Asp Ile Phe
1449     530             535             540
1451 Pro Tyr Gln Val Tyr Arg Gly Cys Leu Arg Ile Asp Gly Gln Thr Met
1452 545             550             555             560
1454 Val Asn Leu Glu Ile Phe Asn Asn Ser Cys Asp Gly Gly Pro Ser Gly
1455         565             570             575
```

```
1457 Thr Leu Tyr Lys Tyr Leu Asp Asn Cys Val Ser Pro Thr Gly Lys Arg
1458             580             585             590
1460 Leu Leu Arg Asn Trp Ile Cys His Pro Leu Lys Asp Val Glu Ser Ile
1461         595             600             605
1463 Asn Lys Arg Leu Asp Val Val Glu Glu Phe Thr Ala Asn Ser Glu Ser
1464     610             615             620
1466 Met Gln Ile Thr Gly Gln Tyr Leu His Lys Leu Pro Asp Leu Glu Arg
1467 625             630             635             640
1469 Leu Leu Gly Arg Ile Lys Ser Ser Val Arg Ser Ser Ala Ser Val Leu
1470             645             650             655
1472 Pro Ala Leu Leu Gly Lys Lys Val Leu Lys Gln Arg Val Lys Ala Phe
1473         660             665             670
1475 Gly Gln Ile Val Lys Gly Phe Arg Ser Gly Ile Asp Leu Leu Leu Ala
1476         675             680             685
1478 Leu Gln Lys Glu Ser Asn Met Met Ser Leu Leu Tyr Lys Leu Cys Lys
1479         690             695             700
1481 Leu Pro Ile Leu Val Gly Lys Ser Gly Leu Glu Leu Phe Leu Ser Gln
1482 705             710             715             720
1484 Phe Glu Ala Ala Ile Asp Ser Asp Phe Pro Asn Tyr Gln Asn Gln Asp
1485             725             730             735
1487 Val Thr Asp Glu Asn Ala Glu Thr Leu Thr Ile Leu Ile Glu Leu Phe
1488             740             745             750
1490 Ile Glu Arg Ala Thr Gln Trp Ser Glu Val Ile His Thr Ile Ser Cys
1491         755             760             765
1493 Leu Asp Val Leu Arg Ser Phe Ala Ile Ala Ala Ser Leu Ser Ala Gly
1494         770             775             780
1496 Ser Met Ala Arg Pro Val Ile Phe Pro Glu Ser Glu Ala Thr Asp Gln
1497 785             790             795             800
1499 Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys Ile Gln Gly Leu Trp His
1500             805             810             815
1502 Pro Phe Ala Val Ala Ala Asp Gly Gln Leu Pro Val Pro Asn Asp Ile
1503             820             825             830
1505 Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly Ser Ile His Pro Arg Ser
1506         835             840             845
1508 Leu Leu Leu Thr Gly Pro Asn Met Gly Gly Lys Ser Thr Leu Leu Arg
1509         850             855             860
1511 Ala Thr Cys Leu Ala Val Ile Phe Ala Gln Leu Gly Cys Tyr Val Pro
1512 865             870             875             880
1514 Cys Glu Ser Cys Glu Ile Ser Leu Val Asp Thr Ile Phe Thr Arg Leu
1515             885             890             895
1517 Gly Ala Ser Asp Arg Ile Met Thr Gly Glu Ser Thr Phe Leu Val Glu
1518             900             905             910
1520 Cys Thr Glu Thr Ala Ser Val Leu Gln Asn Ala Thr Gln Asp Ser Leu
1521         915             920             925
1523 Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr Phe Asp Gly Tyr
1524     930             935             940
1526 Ala Ile Ala Tyr Ser Val Phe Arg His Leu Val Glu Lys Val Gln Cys
1527 945             950             955             960
1529 Arg Met Leu Phe Ala Thr His Tyr His Pro Leu Thr Lys Glu Phe Ala
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Input Set : A:\09529239SeqList.txt
Output Set: N:\CRF3\06122001\I529239.raw

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·1530                965              970              975
 1532 Ser His Pro Arg Val Thr Ser Lys His Met Ala Cys Ala Phe Lys Ser
 1533                980              985              990
 1535 Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp Gln Asp Leu Val Phe Leu
 1536                995              1000             1005
 1538 Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu Ser Tyr Gly Leu Gln Val
 1539     1010             1015             1020
 1541 Ala Leu Met Ala Gly Ile Pro Asn Gln Val Val Glu Thr Ala Ser Gly
 1542 1025             1030             1035             1040
 1544 Ala Ala Gln Ala Met Lys Arg Ser Ile Gly Glu Asn Phe Lys Ser Ser
 1545                1045             1050             1055
 1547 Glu Leu Arg Ser Glu Phe Ser Ser Leu His Glu Asp Trp Leu Lys Ser
 1548                1060             1065             1070
 1550 Leu Val Gly Ile Ser Arg Val Ala His Asn Asn Ala Pro Ile Gly Glu
 1551     1075             1080             1085
 1553 Asp Asp Tyr Asp Thr Leu Phe Cys Leu Trp His Glu Ile Lys Ser Ser
 1554     1090             1095             1100
 1556 Tyr Cys Val Pro Lys
 1557 1105
```

E--> 1542

(handwritten annotations)

Amino acid number cannot be under the amino acids. Move one space to the right

↓ Gly 1040

Remaining lines are shown as erred due to the one error at amino 1040.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:976 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1385 Found:2188 SEQ:26
L:1022 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:28 differs::
L:1542 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
M:332 Repeated in SeqNo=31